

1 DCGAGAGCCCGGAGTGAG TAGCAGCTGGCAAACCCAGGGTAGAAATTCGTCTTCACTTCAAGACTAGGACCATAATGATGCCAA  
 12  
 101 AATTACATAACCGCTGGGTTCAAGGAATATCAGATAAAATCTAACAGGAGATGGCAGACCATTAAGATGGTTGCAAACTTATGCATATC  
 45  
 201 GACCAAGACCTGAGAAAGGAGCTTATTTAACCTAGCTTACATCTCTCTTCAACCATCTGAAAGAATGTTCCATAC  
 79  
 301 TGGTAGCTGCTGCCTGCCTGATATTTAACCTGAGCTCTGAGCCTTACACATCCCCTGATAACAAAGGAAATATTTATGTTATAACAG  
 112  
 401 ACAGTTGAAAGGGCTAGAGGATACAAAGAGCCACAAATTCAGGATTTTACATCTGAGACACATGCTGGGTCAGTCATAAACTATGCTTAC  
 145  
 501 CAGTTAGAAAGATACCAATGAAATTTACCCAGCTATAACAGACCTTATTTCACTTAAACAATGCCACAAATCAGAAAGTCCATATGCTCAC  
 179  
 601 ACCTTATGAGCTCTATTATTTGAGGTGATACAGTGTCTGAGGAGCTTGGATACGGGTTACTAAATCTGGTACCTGCTCATAGAAATTAAACAA  
 212  
 701 GCAAGCATATGATTGGCAAAAGCTTACAGAGAGGACAGCTAACGCTTAACTTAAACAAATGTTTACAGGTTCTGATGCTGGGAA  
 245  
 801 ACATCTACGGCTTTGCTCAGACCATGTTGGACTTAATTTGGAGCTCTACAAATATGAGTCATITGCTGCTCTGTTTACCCAGCTTCA  
 279  
 901 TTAATTAAAGGAAATGAAATGAGGAGGCTACAGTGTAAACTACGGAAAAATGTTGGGCAAGGATTCAGAAATGGCTCTCAAAACAA  
 312  
 1001 GCCACTTTGGCAGTGCTACTTGGCAGGTTAATGATATGCTACCAATGCCCTGGGATGCTGAAATTGGCTAGCCATTGCTCAAGGACATCC  
 345  
 1101 GATTTAGCAAAAGACTTAAAGAGTATCTAAAGTCAAGGACATCACCTCAGGAGCTTAAAGACATGTTATGCTGCTCAAGGACATCC  
 379  
 1201 AAAGGAAATCTTCTGGCTCAATGATCACATGTTAACTTGTGAGAGAGGAAACATTAGACAAACGATGGAGCTTCAAGGAAATGGCTG  
 412  
 1301 TGCCAAATATAAGAAATGCTTACGAGGCTTGGCTCATACGGATGGCTGAAACAGATAGGATCAAAGACAAATTCTACATATATT  
 445  
 1401 CAAAATAGTATTGATCATCGACTACTTGCTGACGGCTTGGCTCATACGGATGGCTCACAATTAGAAACACTACAGAACGGATGAAATGCTT  
 479  
 1501 ACTTGATGCCCCACACTGGAAATTATGCTGAAACCATGAAATGCTGGAAATGCTGGGAAATGCTGGGAAATGCTGGGAAATGCTGG  
 512  
 1601 GATTAAGGAAACCAAAACAGTCAGTCAGGCTCAAGGGCATATTTCAAAAGTGTGTTTACAGAAATGCTGGGAAATGCTGGGAAATGCT  
 545  
 1701 ATGAAAGAAATTCACACAGGTGTTAGAAGAATGAGGAAATAAGAAGGAGTTACAGGATGCTGGGAAATGCTGGGAAATGCTGGGAAATGCT  
 579  
 1801 GTGTCGGTGAATAACTAAAGTTGGGCAACCCAAACAGCTTACAAACGCTTCTGGGAAATGCTGGGAAATGCTGGGAAATGCTGGGAAATGCT  
 612  
 1901 CATAGATACCCAAATCTATGCTCTTAAACAAAGTGAACAAATCAATAGCTGGAAACGGACATGAAAGATGAGGGTGTCCAACTGATCA  
 645  
 2001 ATCACAGGAGCTCTGAACTCTTAAAGCTCTTACATGCTGCTTACACATECCATCTCATTCATGCTGAAACATTCATGCTGCTGCT  
 679  
 2101 TGGATGATGAAAAAGTACGCAAGCTGCACTACAAATTCTGGAAACAGGAAAGCTTGGAAATGCTGCTGAAACATTCATGCTGCTGCT  
 712  
 2201 TGTGTTACATCACAAATCTAAAGGACCCCCCGCTCAAGGAAATATGCCATTCATGCTGCTGAAACATTCATGCTGCTGCTGCTGCT  
 745  
 2301 CAGATATTGAGGCTCTGCTAAAGGCTACATGCTGAAACCTGGAACTCTGGAAATGCTGCTGAAACATTCATGCTGCTGCTGCTGCT  
 779  
 2401 ATCAATTGCTGCTTGGAAATCTGGCTAGCTACTTCTGCTGAAAGATCTGCTGCTGAAATGCTGCTGCTGCTGCTGCTGCTGCT  
 812  
 2501 CGTCCAGATGAAGAAGTATCTCTGAGCAAAATGCTGCTGAAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT  
 845  
 2601 TCAGGAACTCTACCTTAAGGATGCTAACAAACATATTGCTGAGTGTGAGGACTTCAGAGAACAGGGGAAATGCTGCTGCTGCTGCTGCT  
 879  
 2701 GACTTGCTGCTGGGAGTCTATTGCTGAAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT  
 912

FIG. 1-1

**FIG. 1-2**

161

55 LYLNLAH~~L~~ASDFF~~L~~KHPGKDVRLLVACC~~L~~ADIFR~~I~~YAPEAP~~Y~~TSPDK~~L~~KDIFMF~~I~~TRQLKG~~L~~

277

196 217 241 277  
LDTVLVN~~L~~VPAHKN~~L~~NKQAYD~~L~~ MMLGKTS~~I~~SDLSEH~~V~~FDLILELYNIDSH~~L~~LLSVLPQL

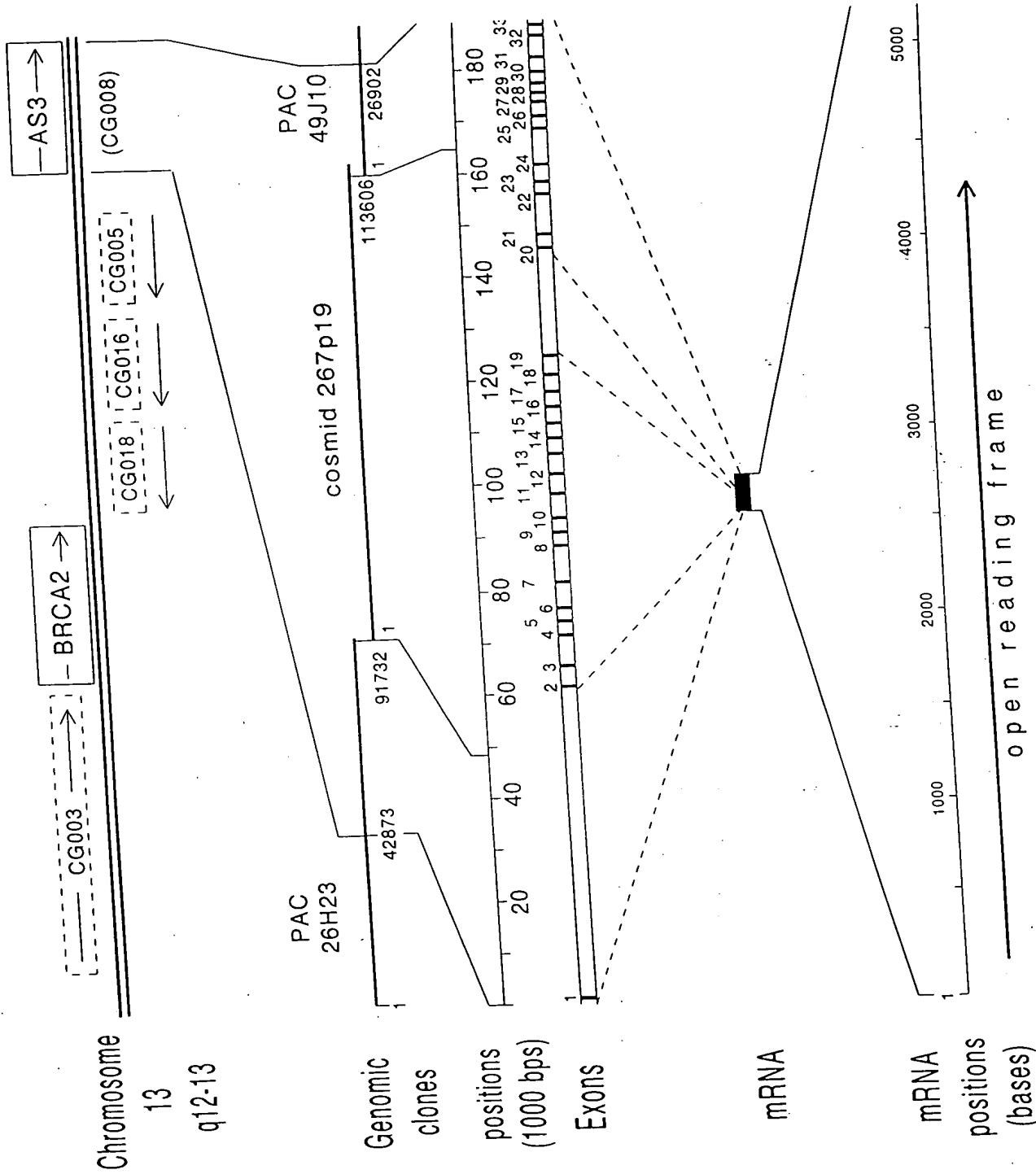
404

319 355 375 404  
LGRFNDIH~~V~~PIRLEC~~V~~KFASHC~~L~~MNH~~P~~D~~L~~A~~K~~DLTEY~~L~~ VTAAKKD~~I~~LLVNDH~~L~~LN~~F~~VRERT~~L~~DKRW~~R~~V

FIG. 2

| Hank's<br>conserved<br>regions:              | Subdomain I   | Subdomain II   | Subdomain III  |
|--|---|--|--|
| Consensus:<br>AS3 position:<br>AS3 sequence: | <p><math>\beta</math>-strand 1<br/>YALQ . SA</p> <p><math>\beta</math>-strand 2<br/>(G x G x x G x V)<br/>426</p> <p><math>\beta</math>-strand 3<br/>(x x x K x x x)<br/>472</p> <p><math>\alpha</math>-helix C<br/>(x x x E x x x)<br/>489</p> <p>VKALN E MWKC</p> | <p><math>\beta</math>-strand 2<br/>453</p> <p>LVERIF</p> <p><math>\beta</math>-strand 3<br/>(x x x K x x x)<br/>472</p> <p>ERM K CLYYLYA</p> | <p><math>\alpha</math>-helix C<br/>(x x x E x x x)</p> <p>QAFKN E MQVL (Araf)</p> <p>TLALN E RIML (bARK1)</p> <p>YTRVR E IKFI (SMEI)</p> |
| Similar<br>protein<br>kinase<br>sequences:   | <p>YTLGVSA (Elm1)</p> <p>YALINLL (Tsl)</p> <p>YHLQNI (Cdc15)</p> <p>YKLVRKI (CK1a)</p> <p>IYIQUESTI (Akt5)</p>  | <p>GeDrfGkV (Rot2)</p> <p>GsGsfGdI (CK1a)</p> <p>AeGesHiS (Ypka)</p> <p>HeSdfSeV (Mik1)</p>  | <p>LLYELMD (YK1516)</p> <p>YLGEQVS (PKN2)</p> <p>YLCCLCN (BCK1)</p> <p>VAI K CIAKKAL (CamK1)</p>   |
| Consensus:<br>AS3 position:<br>AS3 sequence: | <p><math>\beta</math>-strand 4<br/>LLDLIKQP</p> <p><math>\beta</math>-strand 5<br/>IFSK . VMV</p>   | <p><math>\beta</math>-strand 4<br/>509</p> <p><math>\beta</math>-strand 5<br/>525</p>  | <p><math>\alpha</math>-helix D<br/>540</p> <p>GRAQDFMKK</p> <p><math>\alpha</math>-helix E<br/>554</p> <p>EDDEKIRKQ . LEVL</p>           |
| Similar<br>protein kinase<br>sequences:      | <p>LLDIVKDP (TPCKII)</p> <p>LLDWFERP (Pim1)</p> <p>LLGLCREA (Klg)</p> <p>LVKLIGYC (APK1)</p>  | <p>IFSCLVME (PvpK1)</p> <p>KFSCLVME (G11a)</p> <p>KFSCLVME (ZmPPK)</p>   | <p>ERDADAVKQILEA ((CaMKIV)</p> <p>ECDANIMKQILSG (PfCPK)</p> <p>ADQLNIAKQISAG (TORRTK)</p> <p>ESVIMYTKQLL (NPK1)</p>                      |
| Hank's<br>conserved<br>regions:              | Subdomain IV  | Subdomain V  | Subdomain VIa  |

**FIG. 3**



54287 1 46 (42919)  
 CCGGAGAG.... Exon 1 ....ACCCGGAG \* [REDACTED] gaga  
 3347) 47 173 (475)  
 ....ttttcttgcccttag \* GGGTAGAA.... Exon 2 ....GATTAAG \* [REDACTED] gagta...  
 (16397) 174 377 (16602)  
 ..ttttatTTTgtatag \* ATGGTTGT.... Exon 3 ....AACTAAAG \* gcaagta...  
 (22832) 378 464 (22920)  
 ..ctttttttatTTAAG \* GATATATT.... Exon 4 ....TACTTGAG \* gtaagca...  
 (23028) 465 562 (23125)  
 .....ccttatttttag \* AACATTGC.... Exon 5 ....GTTATAAA \* gtaagtt...  
 (23747) 563 689 (23873)  
 ....tttgaatttcgag \* CAATGGCC.... Exon 6 ....CTCATAAG \* gtgagta...  
 (32357) 690 854 (32439)  
 ....tttatgttttcag \* AATTTAAA.... Exon 7 ....TTACCACT \* gtaagtc...  
 (37809) 855 911 (37951)  
 ....cttctccctaaag \* TTTTTAA.... Exon 8 ....AATTAAAG \* gtaactt...  
 (40437) 912 1027 (40554)  
 .....tttatTTTtag \* AGCAATGA.... Exon 9 ....TTGGGCAG \* gatatg...  
 (43428) 1028 1122 (43524)  
 ...tttatTTTTCAG \* GTTAAATG.... Exon 10....CTTAACAG \* gtaactat...  
 (48471) 1123 1268 (48617)  
 ....tgttatcttcag \* AGTATCTT.... Exon 11....ACAAACGA \* gtaagta...  
 (51727) 1269 1420 (51880)  
 ....ttttgttttaag \* TGGAGAGT.... Exon 12....GATGATCG \* gtaagtt...  
 (53049) 1421 1534 (53164)  
 ...tctgcTTTTtag \* ACTACTTG.... Exon 13....GCTGTGAA \* gtagtt...  
 (58816) 1535 1616 (58898)  
 ....tttgcTTTTtag \* AGCATTGA.... Exon 14....AACCCAAA \* gtaagta...  
 (61447) 1617 1665 (61497)  
 ...ttgtgtgatTTacag \* ACAGATGC.... Exon 15....TATTACAA \* gtaagtt...  
 (64323) 1666 1805 (64464)  
 .....tttatttttaag \* GAAATTAA.... Exon 16....GTTGTGTG \* gtaagga...  
 (65916) 1806 1921 (66033)  
 ...taatctgtattacag \* CGTGAAAT.... Exon 17....TCTATCAG \* gtatttg...  
 (71527) 1922 2027 (71633)  
 ...ttggcatatTTtag \* TGCTCTTA.... Exon 18....TGCTTAAG \* gtaagta...  
 (74539) 2028 2188 (74700)  
 ...tgattcatTTtag \* GTACTCTC.... Exon 19....ATCAGATC \* gtgagtt...  
 (96694) 2189 2312 (96818)  
 ....tttttttaatag \* AGCCTTGC.... Exon 20....TATTGAG \* gtaatga...  
 (99765) 2313 2471 (99925)  
 ...tcccctcattttcag \* CCTCTGCA.... Exon 21....ATGATCGG \* gtaattt...  
 (105674) 2472 2540 (105744)  
 ...ctcgTTatTTtag \* CTTCCAGG.... Exon 22....TGGTCAAA \* gtgagta...  
 (107185) 2541 2677 (107322)  
 ...ttgtcttttaatag \* ATTCAAGGC.... Exon 23....AAAATTAG \* gtagc...  
 (110571) 2678 2801 (110696)  
 ...ctactcattttcag \* TAAACCAG.... Exon 24....CTATCAAC \* gtaagga...  
 [4319] 2802 3006 [4524]  
 ....ttgtgtctttacag \* GATGAATG.... Exon 25....TGTTAGTG \* gtaagca...  
 [6829] 3007 3121 [6945]  
 ....tttctttttcag \* AAAAATTA.... Exon 26....GTTAAAGA \* gtaagac...  
 [9074] 3122 3254 [9208]  
 ....tttttttttttag \* ATGTCTT.... Exon 27....TGAATGAA \* gtatgt...  
 [9522] 3255 3374 [9642]  
 ....tatactatttcag \* AAACGTGA.... Exon 28....CTGACAAG \* gtagtta...  
 [10614] 3375 3437 [10679]  
 ...ttctctggTTtag \* AATTCAG.... Exon 29....CTGGAAAA \* gtatgt...  
 [11561] 3438 3583 [11709]  
 ...cattctcattttcag \* CCTAAAC.... Exon 30....AAGGGGAG \* gtaagt...  
 [15476] 3584 3689 [15583]  
 ...tgtctgtatTTaaag \* GCTTGATA.... Exon 31....TTGTAAGG \* gtgagat...  
 [21107] 3690 4129 [21548]  
 ....ttttttttccctag \* TCTGAATT.... Exon 32....CAGCAGAG \* gtaagca...  
 [21640] 4130 4354 [21866]  
 ...tctccccaaagcag \* AGCAGAAT.... Exon 33....TACACTAG \* gtaagat...  
 [26002] 4355 5253 [26902]  
 ....cttccTTtaag \* GTACGGCG.... Exon 34....GAATGAGT \* (poly-A)

**FIG. 5**

1 CGGAGAGGAGGAGGAACGGCAGGGCTGGCTGCCAAGGGGAGGGGGGGAGAAGGCAGTTGGATGCCCGCGGCCGATCCGGAGAGCCCCGGAG  
 101 TGACCGGAGTAGCGAGTCGGCAACCGGAGGGTAGAAATATTCTGTATGGCTCATGGCTTACAAAGACTAGGACCAATGATGGAAAAATTACATATCCGCT  
MetAlaHisSerLysThrArgThrAspGlyLysIleThrThrProPro 17  
 201 GGGGTCAGGAAATATCAGATAAAATCTAAAGGGAGATGGTGAGACGATAAAAGATGGTGTGAAACATTATGGATATGGACCAAGGACTCTGAAG  
GlyValLysGluIleSerAspLysIleSerLysGluGluMetValArgArgLeuLysMetValValLysThrPheMetAspMetAspGlnAspSerGluG 51  
 301 AAGAAAAGGAGCTTATTAAACCTAGCTTACATCTTGCTCAGATTTCTCAAGCATCTGGTAAGAGATGTTGCTACTGGTAGCCTGCTGCCT  
luGluLysGluLeuTyrLeuAsnLeuLeuAlaSerAspPhePheLysHisProGlyLysAspValArgLeuLeuValAlaCysCysLe 84  
 401 TGCTGATATTCAGGATTATGCTCCTAACACCCCCGATAAAACTAAAGGATATATTATGTTATAACAAGACAGTTGAAGGGCTA  
uAlaAspIlePheArgIleTyrAlaProGluAlaProTyrThrSerProAspLysLeuLysAspIlePheMetPheIleThrArgGlnLeuLysGlyLeu 117  
 501 GAGGATACAAAGAGCCCACAATTCAATAGGTTTTACTTGAGAACATGCTGGCTCAAGTCATATAACATATGCTTGAGTTAGAAGATAGCA  
GluAspThrLysSerProGlnPheAsnArgTyrPheTyrLeuLeuGluAsnIleAlaTrpValLysSerTyrAsnIleCysPheGluLeuGluAspSerA 151  
 601 ATGAAATTTACCCAGCTATACAGAACCTTATTTCAAGTATAAACATGGCCACAATCAGAAAAGTCCATATGCACATGGTAGACCTTATGAGCTCTAT  
snGluIlePheThrGlnLeuTyrArgThrLeuPheSerValIleAsnAsnGlyHisAsnGlnLysValHisMetValAspLeuMetSerSerI 184.  
 701 TATTGTGAAGGTGATACTGCTCAGGGCTTGGATACGGTTAGTAAATCTGTCACCTGCTCATAAAGAATTAAACAAGCAAGCATATGATTG  
eIleCysGluGlyAspThrValSerGlnGluLeuLeuAspThrValLeuValAsnLeuValProAlaHisLysAsnLeuAsnLysGlnAlaTyrAspLeu 217  
 801 GCAAAGGCTTACTGAAGAGGACAGCTCAAGCTATTGAGCCATATAACCCTTTAACTCAGGTTCTGATGCTGGGAAACATCTATCAGCATT  
AlaLysAlaLeuLeuLysArgThrAlaGlnAlaIleGluProTyrIleThrPhePheAsnGlnValLeuMetLeuGlyLysThrSerIleSerAspL 251  
 901 TGTCAGAGCATGCTTGGACTTAATTGGCTCTACAATATTGATGACTTGTCTCTGTTACCCAGCTGAAATTAAAGAGCAA  
euSerGluHisValPheAspLeuIleLeuGluLeuTyrAsnIleAspSerHisLeuLeuLeuSerValLeuProGluLeuGluPheLysLeuLysSerAs 284  
 1001 TGATAATGAGGAGGCCACAAGTTAAACTACTGGCAAAAGGATTAGAATTGGCTCTCAAACAAAGCCACTTGGCAGTGC  
nAspAsnGluGluArgLeuGlnValValLysLeuLysAspSerGluLeuAlaSerGlnAsnLysProLeuTrpGlnCys 317  
 1101 TACTGGCAGGTTAATGATATCCATGTACCATCCGCTGGATGTTGAAATTGCTAGCCATTGTCATGAACCCTCTGATTAGC  
TyrLeuArgPheAsnAspIleHisValProIleArgLeuGluCysValLysPheAlaSerHisCysLeuMetAsnHisProAspLeuAlaLysAspL 351  
 1201 TAACAGAGTACTTAAAGTGGGGTACATGACCTGGAGAACGATTAGACATGATGTTATTGTCATAGCTGCTAAAAAGGATATTCTTCT  
euThrGluTyrLeuLysValArgSerHisAspProGluGluAlaIleArgHisAspValIleValThrAlaAlaLysAspIleLeuLe 384  
 1301 GGTCATGACTACTTAAATTGAGAGAGAGAACATTAGACAAACGATGGAGAGTACGCAAAGAACCCATGATGGACTGCCAAATTATAAG  
uValAsnAspHisLeuLeuAsnPheValArgGluArgThrLeuAspLysArgTrpArgValArgLysGluAlaMetMetGlyLeuAlaGlnIleTyrLys 417  
 1401 AAATATGCTTACAGTCAGCAGCTGGAAAAGATGCTGCAAACAGATAGCATGGATCAAAGACAAATTGCTACATATATATCAAATAGTATTGATG  
LysTyrAlaLeuGlnSerAlaAlaGlyLysAspAlaAlaLysGlnIleAlaTrpIleLysAspLysLeuLeuHisIleTyrTyrGlnAsnSerIleAspA 451  
 1501 ATCGACTACTTGTGAACGGATTTGCTCAATACATGGTCTCACAATTAGAACACTACAGGATGAAATTGCTTACTTGTGCTATGCCACACT  
spArgLeuLeuValGluArgIlePheAlaGlnTyrMetValProHisAsnLeuGluThrPheArgMetLysCysLeuTyrTyrLeuTyrAlaThrLe 484  
 1601 GGATTTAAATGCTGAAAGCATTGAATGAAATGTCGAAACATCTGCTCCGACATCAAGTAAAGGATTGCTGACTTGTGATTAAGCAACCCAAA  
uAspLeuAsnAlaValLysAlaIleAsnGluMetTrpLysCysGlnAsnLeuLeuArgHisGlnValLysAspLeuLeuAspIleLysGlnProLys 517  
 1701 ACAGATGCCAGTGTCAAGGCCATTTCAGGAAATTGTTTACAGGAAATTGCTGATCTGGTAAGGCTCAGGATTTCATGAAGAAATTCACAC  
ThrAspAlaSerValAlaIleSerLysValMetValIleThrArgAsnLeuProAspProGlyLysAlaGlnAspPheMetLysPheThrG 551  
 1801 AGGTGTTAGAAGATGATGAGAAAATAAGAACGATTAGAAGTACTTGTGTTAGCCAACATGCTCTGCAAGCAGGCTGAAGGTTGTCGCTGAAATTAC  
InValLeuGluAspAspGluLysIleArgLysGlnLeuGluValLeuValSerProThrCysSerCysLysGlnAlaGluGlyCysValArgGluIleTh 584  
 1901 TAAGAAGTTGGCAACCCCAACAGCCTACAAATCTTCTGGAAATGATCAAGTTCTCTGGAGAGGATAGCACCTGTGCACATAGATACCGAATCT  
rLysLysLeuGlyAsnProLysGlnProThrAsnProPheLeuGluMetIleLysPheLeuLeuGluArgIleAlaProValHisIleAspThrGluSer 617  
 2001 ATCAGTGTCTTAAACAGTGAACAAATCAATAGATGAAACAGCAGATGATGAAGATGAGGGTGTCCAACCTGATCAAGCCATCAGAGCAGGTCTG  
IleSerAlaLeuIleLysGlnValAsnLysSerIleAspGlyThrAlaAspAspGluAspGluGlyValProThrAspGlnAlaIleArgAlaGlyLeuG 651  
 2101 AACTGCTTAAGGTACTCTCATTTACACATCCATCTCATTCTGTCAGAACATTGAAATCTGCTTGTGCTGAAATGGATGATGAAAAAGT  
IleLeuLeuLysValLeuSerPheThrHisProIleSerPheHisSerAlaGluMetIleLysPheLeuLeuAlaCysLeuLysMetAspAspGluLysVa 684  
 2201 AGCAGAAGCTGCACTACAAATTTCAGGAAACGAGGAAATTGAAGAGGATTTCACACATCAGATCAGGCCCTGCTCCTGTTACATCACAAA  
1AlaGluAlaAlaLeuGlnIlePheLysAsnThrGlySerLysIleGluGluAspPheProHisIleArgSerAlaLeuLeuProValLeuHisLys 717  
 2301 TCTAAAAAAGGCCAGGCCAGGCCAGCCAAATGCCATTGCTATCCATTGCTATGCCATTGCTATGCCATTGCTATGCCATTGCTATGCCATTGCT  
SerLysLysGlyProProArgGlnAlaLysSerTyrAlaIleHisCysIleHisAlaIlePheSerSerLysGluThrGlnPheAlaGinIlePheGluProl 751  
 2401 TGCTATAAGGCCAGTCAAGCAGCACCTGAGACATCTCATGAAACCATGCTCATGAAACCATGGTACTATTGCTCATATTGCTCTCTGCACTGATCA  
euHisLysSerLeuAspProSerAsnLeuGluHisIleLeuIleThrProLeuValThrIleGlyHisIleAlaLeuLeuAlaProAspGlnPheAlaAlaPr 784  
 2501 TTGGAAATCTGGTAGCTTCTCATGAAAGATCTCTCATGAAATGATCGGCTTCCAGGGAAAAGACAACTAAACATTGGTCTCAGATGAAGAA  
oTrpLysSerTrpValAlaThrPheIleValLysAspLeuLeuMetAsnAspArgLeuProGlyLysLysThrLysLeuTrpValProAspGluGlu 817  
 2601 GTATCTCTGAGACAATGTCAAAATTCAAGCTATTAAATGATGGTTCGATGGCTACTTGGAAATGAAAATAATCACAGTAAATCAGGAACTTCTACCT  
ValSerProGluThrMetValLysIleGlnAlaIleLysMetValArgTrpLeuLeuGlyMetLysAsnAsnHisSerLysSerGlyThrSerIle 851  
 2701 TAAGATTGCTAACACAAATTGCTAGTGTGAGACTTGAGAGAACAGGGAAAATTAGTAAACACAGATATGTCACGCTGAGACTTGCTGCTGGAG  
euArgLeuLeuThrThrIleLeuHisSerAspGlyAspLeuThrGluGlnGlyLysIleSerLysProAspMetSerArgLeuArgLeuAlaGlySe 884  
 2801 TGCTATTGTGAAGCTGGCACAAGAACCTGTTACCATGAAATCATCACATAGAACAAATCAGCTATGTCATTAGCTATCAACAGTGAATGCTATCAA  
rAlaIleValLysLeuAlaGlnGluProCysTyrHisGluIleIleThrLeuGluGlnTyrGlnLeuCysAlaLeuAlaIleAsnAspGluCysTyrGln 917  
 2901 GTAAAGACAAGTGTGCCCCAGAAACTCACAAAGGCCCTTCCGTTACGGCTTCCACTGAGTATGCAAGCAGCATGCCGAGTCTGCTGTTAGTGA  
ValArgGlnValPheAlaGlnLysLeuHisLysSerArgLeuArgLeuProLeuGluTyrMetAlaIleCysAlaLeuAsnAspProv 951  
 3001 TAAAGGAGAGAGAGGCTCATGCTAGGCAATGTTGGTGAAGAAATAATGTAAGGGGGAGATCTCAAGCAGCATGCGAGTCTGCTGTTAGTGA  
allysGluArgArgAlaHisAlaArgGlnCysLeuValLysAsnIleAsnValArgArgGluTyrLeuLysGlnHisAlaAlaValSerGluLysLeu 984  
 3101 GTCTCTTCTACCGAGATGTFGTCCATATCATATTACACCTTTGGCACATGACCCAGATTATGTCAGAAGTACAGGATTGAAACAACCTAAAGATGTT  
uSerLeuLeuProGluTyrValValProTyrThrIleHisLeuLeuAlaHisAspProAspPheTyrValLysValGlnAspIleGluGlnLysAspVal 1017  
 3201 AAAGAATGTCCTGGTTCTGGAAATATTAATGGCTAAAATGAAATAACAGTCAGCCTTATGAGAAATGGTAGAAATAACAAACAA  
LysGluCysLeuTrpPheValLeuGluIleLeuMetAlaLysAsnGluAsnAsnSerHisAlaPheIleArgLysMetValGluAsnIleLysGlnThrL 1051

**FIG. 6-1**

3301 AAGATGCCAAGGACCAG GCAAAAATGAATGAAAAACTGTACACTGTGTGTATGTTGCCTTATCATCATGTCAAAGAGTACTACATACAG  
 ysAspAlaGlnGlyProAsp AlaLysMetAsnGluLysLeuTyrThrValCysAspValAlaMetAsnIleIleMetSerLysSerThrThrTyrSe 1084  
 3401 TTTGGAAATCTCTAAAGACCCGGTACTACCAGCTCGTTCTTCACTCACCTGACAAGAATTTCAGTAACCAAAAATTATCTGCCTCCTGAAATGAAA  
 rLeuGluSerProLysAspProValLeuProAlaArgPheThrGlnProAspLysAsnPheSerAsnThrLysAsnTyrLeuProProGluMetLys 1117  
 3501 TCATTTTCACTCCTGGAAACCTAAAACAACCAATGTTAGGAGCTGTTAACAGCCACTTCATCAGCAGGCAAGCAATCTCAGACCAAATCATCAC  
 SerPhePheThrProGlyLysProLysThrAsnValLeuGlyAlaValAsnLysProLeuSerSerAlaGlyLysGlnSerGlnThrLysSerSerA 1151  
 3601 GAATGGAAACTGTAAAGCAAGCAGCAGCTCAAATCCAAGCTCTCCTGGAAGAATAAAGGGGAGGCTTGATAGTTCTGAAATGGATCACAGTGAAA  
 rgMetGluThrValSerAsnAlaSerSerAsnProSerSerProGlyArgIleLysGlyArgLeuAspSerSerGluMetAspHisSerGluAs 1184  
 3701 TGAAAGATTACACAAATGCTTCACCTTGCCTGGGGAAAAAAAGTGACAAGAGAGACGACTCTGATCTGTAAGGTCTGAATGGAGAAGCCTAGAGGCAGG  
 nGluAspTyrThrMetSerSerProLeuProGlyLysLysSerAspLysArgAspAspSerAspLeuValArgSerGluLeuGluLysProArgGlyArg 1217  
 3801 AAAAACGCCCCGTACAGAACAGGAGGAGAAATTAGGTATGGATGACTTGACTAAGTTGGTACAGGAACAGAAACCTAAAGGCAGTCAGCGAAGTCGGA  
 LysLysThrProValThrGluGlnGluLysLeuGlyMetAspAspLeuThrLysLeuValGlnGluGlnLysProLysGlySerGlnArgSerArgL 1251  
 3901 AAAAGGGCCATACGGCTTCAGAATCTGATGAAACAGCAGTGGCTGAGGAAAGAGGCTAAAGAAGATATAATTAGAAAATGAAAGATGAAACAGAATAGTCC  
 ysArgGlyHisThrAlaSerGluSerAspGluGlnGlnTrpProGluGluLysArgLeuLysGluAspIleLeuGluAsnGluAspGluGlnAsnSerPr 1284  
 4001 GCCAAAAAAGGGTAAAGAGGCCGACCACCAAAACCTCTGGTGGAGGTACACCAAAAGAAGAGCCAACATGAAAACCTCTAAAAAGGAAGCAAAAAA  
 oProLysLysGlyLysArgGlyArgProProLysProLeuGlyGlyThrProLysGluGluProThrMetLysThrSerLysGlySerLysLys 1317  
 4101 AAATCTGGACCTCCGACCCAGAGGAGGAGGAGAAGAAGAACAGACAGTGGAAATACGGAACAGAACAGCAGCAGGTGTCAGGA  
 LysSerGlyProProAlaProGluGluGluGluGluArgGlnSerGlyAsnThrGlnLysSerLysGlnHisArgValSerArgA 1351  
 4201 GAGCACAGCAGAGCAGAACATCTCTGAATCTAGTGAATTGAAATCCACACAGTCCACACACAAAGGACGAGGACCATCAAAAACGCCATCACC  
 rgAlaGlnArgAlaGluSerProGluSerSerAlaIleGluSerThrGlnSerThrProGlnLysGlyArgGlyArgProSerLysThrProSerPr 1384  
 4301 ATCACAAACAAAAAAATGTGTAAGTTGAAATATTACATTCAAACCAATTCAAATTATTTGAAAGTTCTAAATTGTAACACATACATATTG  
 oSerGlnProLysLysAsnValEnd 1391  
 4401 TGATTTAAATTCCATATATTAGCCCCATTACACTAGGTACGGCGCGAAGTCTAAAGGGAAACGGCGATGAACAAATGTAATTAACTTCTG  
 4501 TGAAAGCTTGGAAAAATCTTTTTTTTTTTTTGGTCAAGCTTGAGGCTGAATAAAGCCTTGTGACAAAAATGGACTGCTGAAGAGTGG  
 4601 ACAGTTGGACCTACTTGGTACCCCATACTTGTGGTCACATGCTTAGCCATACACATGGTAACATTGACTATGGAGTCTTGTGAAAGTGTAAATGT  
 4701 GCGATGGCTATGTAGACATAAAAAGAAGAAACTTGTAAATATCTTTTTCTTTTAATGTTCTGATTCTGAAAGTGTCTGTATAGCTTTATCTGCGG  
 4801 CTTAAACTGACAGTACCCGACTGTTATTGGATCTATTGATTGAAAGAATTGTTAGGATAGATCTAACAGCTAACATGTCAGTGTGTTGATTG  
 4901 ATTTCTGCAATTACTGTGAAAAAAATTGTTCAACAATTGGTGTCAATTCTGATGTCACTATTGTTGGAGAGTAAATGGCTCTCCCTT  
 5001 TGTGTATCTTACCTAGTGTACTCCTGGCACCCCTAACCTCAGAGGTGCTAAATTGTCAGGCCATTACACCAGAAGGATGCCCTGATAGGAGGACAA  
 5101 CCATGCAAATTGAAAGTCTGAAAGTCTGGATTACTTACACCTCAGTATTGATTGTCAGGCCATTACACCAGAAGGATGCCCTGATAGGAGGACAA  
 5201 TAAGAAGAAAGATTTAAAGTATTTAATTAAAGAGTGTGTTAAAATAATGACTGAAATTCTTATCCCATTTATCATCCTTCAGTTTATTAA  
 5301 TCTACTGTATCAATAAAATTCTGAAATTGAGTAAAAAAAAAAAAAA (5337)

FIG. 6-2